

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 05-23-03
Searcher: Beverly E 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGN

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 08:37:43 ; Search time 6628 Seconds

(Without alignments)
11086.992 Million cell updates/sec

Title: US-09-993-731-10

Perfect score: 2525
Sequence: 1 cctcggcgtcgtcgtcgc.....cgcattctctcctccacaga 2525

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

rd size : 100

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*

1: gb.ba:*
2: gb.hcg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
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8: gb.pl:*
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37: em.htg.vrt:*
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40: em.htgo.mus:*
41: em.htgo.other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1549	61.3	4501	9	BC008782	BC008782 Homo sapi
2	820	32.5	7543	9	HS8242601	HS8242601 Homo sapi
3	400	15.8	191078	2	AC022505	AC022505 Homo sapi
4	340	13.5	1813	9	HS016258	HS016258 Human 1 kap
c 5	138	5.5	69215	2	AC087337	AC087337 Homo sapi

ALIGNMENTS

RESULT 1
BC008782
LOCUS
DEFINITION
BC008782 4501 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, nuclear factor of kappa light polypeptide gene
enhancer in B-cells inhibitor-like 2, clone MGC:3398 IMAGE:3628374,
mRNA, complete cds.
ACCESSION
BC008782 GI:14250635
VERSION
BC008782.1
KEYWORDS
MGC.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens.
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 4501)
JOURNAL
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://imgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-ref@mail.nih.gov
REMARK
COMMENT
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigrl.nih.gov
Shvchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantrop, S., Thomas, P.J.,
Tongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>
Series: IRAL Plate: 12 Row: C Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7305310.
Location/Qualifiers

FEATURES

SOURCE

1. 4501
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/db_xref="taxon:9606"
/clone="MGC:3398 IMAGE:3628374"
/tissue="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
474. .4133

Pred. No. is the number of results predicted by chance to have a

CDS

QY 2313 GACCTGACCTGAGACGCGGACAGAGCCAGGCGCATGGAGATGCTCTCCAGCGGCT 2372
|||||
Db 1938 GACCTGGACCTGGAGACGCGGACAGAGCCAGGCGCATGGAGATGCTCTCCAGCGGCT 1997
QY 2373 GCCTGCGGCGCCAG 2385
|||||
Db 1998 GCCTGCGGCGCCAG 2010

RESULT 2
HSA249601 7543 bp DNA linear PRI 07-SEP-2000
LOCUS
DEFINITION Homo sapiens partial NFKBIL2 gene for IkappaB, exons 1-13.
ACCESSION AJ249601
VERSION AJ249601.1 GI:6580427
KEYWORDS IkappaB; NFKBIL2 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 7543)
AUTHORS Norman,D.A. and Barton,P.J.
TITLE Isolation, sequence, and chromosomal localisation of the human
IkappaB gene (NFKBIL2)
JOURNAL Ann. Hum. Genet. 64 (Pt 1), 15-23 (2000)
MEDLINE 21141789
PUBMED 11246458
REFERENCE 2 (bases 1 to 7543)
AUTHORS Norman,D.A.M.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1999) Norman D.A.M., Cardiothoracic Surgery,
National Heart and Lung Institute, Dovehouse Street, London, SW3
6LY, UNITED KINGDOM

FEATURES
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location/Qualifiers
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HEPVALLELRGASVTLTRKGLSPLETLQOMVKLYRRDLDETROKARAMEMLQAA
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BASE COUNT 1407 a 2143 c 2547 g 1445 t 1 others
ORIGIN
Query Match 32.5%; Score 820; DB 9; Length 7543;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 CTTGGGCTGTGGCGTGGCCACCGAAGATGAGAGGCGCTGGCGCGGATGAGAGT 60
    |||||
Db 1 CTCGGGCTGTGGCGTGGCCACCGAAGATGAGAGGCGCTGGCGCGGATGAGAGT 60
OY 61 ACCGGCTGTGGCGTGGCCACCGAAGATGAGAGGCGCTGGCGCGGATGAGAGT 120
    |||||
Db 61 ACCGGCTGTGGCGTGGCCACCGAAGATGAGAGGCGCTGGCGCGGATGAGAGT 120
OY 121 GAGCGCTGTGGCGTGGCCACCGAAGATGAGAGGCGCTGGCGCGGATGAGAGT 180
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Db 121 GAGCGCTGTGGCGTGGCCACCGAAGATGAGAGGCGCTGGCGCGGATGAGAGT 180
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Db 181 ACACCTGACCTGACGAGCTTGTCTTACCGCCCGGCGCAGTCCGGTGGAGCC 240
OY 241 ACAGCTTGTCTTACGAGCTTGTCTTACCGCCCGGCGCAGTCCGGTGGAGCC 300
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OY 301 CGTATTATTAGCTGTGTGTGTGTGGGAGAGTCCAGCCCATCCCAAAAGCTTC 360
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OY 361 ACCCTGCTGTGGAGGAGAGTGTCAACCCCGCCCAACTGCCAGTCCCGTCCCA 420
    |||||
Db 361 ACCCTGCTGTGGAGGAGAGTGTCAACCCCGCCCAACTGCCAGTCCCGTCCCA 420
OY 421 CGTGACGCTGTGGAGGAGAGTGTCAACCCCGCCCAACTGCCAGTCCCGTCCCA 480
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Db 421 CGTGACGCTGTGGAGGAGAGTGTCAACCCCGCCCAACTGCCAGTCCCGTCCCA 480
OY 481 GCAAGAGAGGAGGAGGAGTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 540
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Db 481 GCAAGAGAGGAGGAGGAGTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 540
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Db 541 CTTTCTTACCAAGACAGAGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 600
OY 601 GTGGCTTACAGAGGAGTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG 660
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OY 661 CACATTTCTTGGCGGACACAGAGGAGTGTGGGCTGTGGGCTGTGGGCTGT 720
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Db 721 ACCTGACATCTTACGAGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 780
OY 781 TTGAGAGAGCTTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGT 820
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Db 781 TTGAGAGAGCTTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGT 820

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RESULT 3
AC022505
LOCUS AC022505 191078 bp DNA linear HTG 09-MAY-2002
DEFINITION Homo sapiens clone RP11-349C2, WORKING DRAFT SEQUENCE, 21 unordered
pieces.
ACCESSION AC022505
VERSION AC022505.17 GI:20335463
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 191078)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Alshrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarta,J., Benton,J., Bimaye,K., Blankenburg,K., Bonin,D.,
Bouk,J., Bowles,S., Brileva,M., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,K., Dathorne,S.R., David,R.,
Della,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dink,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gottlieb,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Hollaway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hultky,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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Lopez,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,U.,
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Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,
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Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
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Peters,L., Plickens,R., Plickens,E., Plickens,M., Ren,Y.,
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Scheper,E., Scott,G., Shen,H., Shooshitari,N., Sisson,I.,
Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umsni,K., Vaequez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wleciyk,R., Woden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and GDBs.R.

Direct Submission
Unpublished
2 (bases 1 to 191078)
Worley,K.C.
Direct Submission
Submitted (05-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 191078)
Worley,K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117888.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: NHDS
Center clone name: RP11-349C2
Sequencing vector: M13
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 17422 bases at least Q40
Consensus quality: 181742 bases at least Q30
Consensus quality: 186048 bases at least Q20
Estimated insert size: 185777; sum-of-contrigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hugsc.bcm.tmc.edu/docs/genbank/draft_data.html)

NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1	2636:	config of 2636 bp in length
2	2737:	gap of unknown length
3	2737:	2736: config of 2179 bp in length
4	4915:	gap of unknown length
5	5015:	gap of unknown length
6	5016:	5015: config of 2959 bp in length
7	7975:	8074: gap of unknown length
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9	10088:	10187: gap of unknown length
10	10188:	13308: config of 3121 bp in length
11	13309:	13408: gap of unknown length
12	13409:	19072: config of 5664 bp in length
13	19072:	19172: gap of unknown length
14	19173:	23309: config of 4137 bp in length
15	23310:	23409: gap of unknown length
16	23410:	28507: config of 5098 bp in length
17	28308:	28607: gap of unknown length
18	28608:	31965: config of 3358 bp in length
19	31966:	32065: gap of unknown length
20	32066:	38613: config of 6548 bp in length
21	38614:	38713: gap of unknown length
22	44465:	44465: config of 5752 bp in length
23	44466:	44555: gap of unknown length
24	44566:	49194: config of 4629 bp in length
25	49195:	49294: gap of unknown length
26	49295:	58857: config of 9563 bp in length
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28	58958:	66455: config of 7528 bp in length
29	66486:	66585: gap of unknown length
30	66586:	77457: config of 10872 bp in length
31	77458:	77557: gap of unknown length
32	77558:	91545: config of 13988 bp in length
33	91546:	91645: gap of unknown length
34	91646:	107288: config of 15643 bp in length
35	107289:	107388: gap of unknown length
36	107389:	121554: config of 14176 bp in length
37	121565:	121654: gap of unknown length
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39	136970:	137069: gap of unknown length
40	137070:	153597: config of 16528 bp in length
41	153598:	153697: gap of unknown length
42	153698:	191078: config of 37381 bp in length

FEATURES	
source	Location/Qualifiers
1.	1. 191078 /organism="Homo sapiens" /db_xref="taxon:9606" /clone-RP11-349C2" 37980 a 55810 c 56330 g 38874 t 2084 others
BASE COUNT	
ORIGIN	

Query Match	15.8%;	Score 400;	DB 2;	Length 191078;
Best Local Similarity	99.5%;	Pred. No. 4.9e-190;		
Matches 740;	Conservative 0;	Mismatches 2;	Indels 2;	Gaps 2

Oy	70	CTTAGGTGGGGGGCGCCCTACACGAGCTGGCTGGCCAGCCGGGGGCGCTCTGAGACCTTTT	129
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Oy	130	TCTGAGGAGGAGGAGGCTGTGTCTTGTCCCTCAGAGAGCTCGAGGCTGGAGGGAGACCTTGAC	189
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Oy	190	CTGAGCGAGCCTTCTTCACCCGCGCCGGGGCACT-CTCGGTGGGAGACCCCAAGGCTTT	248
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QY	249	TCCTGGGACGTGGGGCAGCAGACTAGGTTTCTCTGGCACACAGAAACCATTAAGCACTATT	308
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QY	309	TAGCTGTGTTTGTGTGGGGGAGGTCCAGGCCCCATCCCAAAAAGCTCTCCGTACCCGTGGC	368
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QY	369	TGCTGGAGGCGAGGACTGGCAACCCGCCGCGCAACTCCACAGCTGGCCCTCCCGACGTGACAG	428
Db	154569	TGCTGGAGGCGAGGACTGGCAA -CCCCGCCGCAACTCCACAGTGGCCCTCCCGACGTGACAG	154627
QY	429	CCTTGGCTGCATACAGCGTGAAGCCACTGTCCACACAGAGAGCCCTTGGCATGACAGGA	488
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QY	489	GGGGACGCTGTGGCCCTTGGCCCTCTGTGGGGGTTAGGGGGAGACAGGCTTTCCTT	548
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QY	549	AGCAAGAACAGAGGCTCTCTGGGAATCTGGCGAGTGCAGGTTTGCTTAGGCGAGTGGCTT	608
Db	154748	AGCAAGAACAGAGGCTCTCTGGGAATCTGGCGAGTGCAGGTTTGCTTAGGCGAGTGGCTT	154807
QY	609	ACAGCAGTGACTTCTTCCACACTGACGACACGACACCAAGTACCTGAGCTGGACATTCC	668
Db	154808	ACAGCAGTGACTTCTTCCACACTGACGACACGACACCAAGTACCTGAGCTGGACATTCC	154867
QY	669	CTGGCCAAACCCACAGGAGCTGAGAGGGGCTTGGGACACATCGGGCGGACCCACCACTGGAC	728
Db	154868	CTGGCCAAACCCACAGGAGCTGAGAGGGGCTTGGGACACATCGGGCGGACCCACCACTGGAC	154927
QY	729	ATCTATGACCACTGCGCAGTGCAGGAGATGTTTGTCTGACAGGACACAGGCTTGTGAGAAG	788
Db	154928	ATCTATGACCACTGCGCAGTGCAGGAGATGTTTGTCTGACAGGACACAGGCTTGTGAGAAG	154987
QY	789	AGCTTGCTATTGTGGATGAGGAG 812	
Db	154988	AGCTTGCTATTGTGGATGAGGAG 155011	

RESULT 4			
LOCUS	HSU16258	1813 bp	mRNA
DEFINITION	Human I kappa B mRNA, complete cds.		
ACCESSION	U16258		
VERSION	U16258.1	GI:746414	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 325 to 1770)		
AUTHORS	Ray, P., Zhang, D.H., Elias, J.A. and Ray, A.		
TITLE	Cloning of a differentially expressed I kappa B-related protein		
JOURNAL	J. Biol. Chem. 270 (18), 10680-10685 (1995)		
MEDLINE	95256234		
PUBMED	7738005		
REFERENCE	2 (bases 1 to 1813)		
AUTHORS	Ray, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-OCT-1994) Anuradha Ray, Internal Medicine/Pulmonary Section, School of Medicine, Yale University, 333 Cedar Street, LCI 105, New Haven, CT 06520-8057, USA		
FEATURES	Location/Qualifiers		
source	1..1813		

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/organism="Homo sapiens"
/db_xref="taxon:3606"
/cell_line="HeLa S3"
1..324
325..1770
/function="inhibitor of transcription factor NF kappa B"
CDS
5'UTR

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* 3144 3243: gap of 100 bp
* 3244 4033: contig of 790 bp in length
* 4034 4133: gap of 100 bp
* 4134 4825: contig of 692 bp in length
* 4826 4925: gap of 100 bp
* 4926 5649: contig of 724 bp in length
* 5650 5749: gap of 100 bp
* 5750 6464: contig of 715 bp in length
* 6465 6564: gap of 100 bp
* 6565 7272: contig of 708 bp in length
* 7273 7372: gap of 100 bp
* 7373 8069: contig of 697 bp in length
* 8070 8169: gap of 100 bp
* 8170 8884: contig of 715 bp in length
* 8885 8984: gap of 100 bp
* 8985 9724: contig of 740 bp in length
* 9725 9824: gap of 100 bp
* 9825 10535: contig of 709 bp in length
* 10534 10633: gap of 100 bp
* 10634 11363: contig of 730 bp in length
* 11364 11463: gap of 100 bp
* 11464 12178: contig of 715 bp in length
* 12179 12278: gap of 100 bp
* 12279 12996: contig of 718 bp in length
* 12997 13096: gap of 100 bp
* 13097 13810: contig of 714 bp in length
* 13811 13910: gap of 100 bp
* 13911 14621: contig of 711 bp in length
* 14622 14721: gap of 100 bp
* 14722 15433: contig of 712 bp in length
* 15434 15533: gap of 100 bp
* 15534 16257: contig of 724 bp in length
* 16258 16357: gap of 100 bp
* 16358 17070: contig of 713 bp in length
* 17071 17170: gap of 100 bp
* 17171 17839: contig of 669 bp in length
* 17840 17939: gap of 100 bp
* 17940 18628: contig of 689 bp in length
* 18629 18728: gap of 100 bp
* 18729 19444: contig of 716 bp in length
* 19445 19544: gap of 100 bp
* 19545 20254: contig of 710 bp in length
* 20255 20354: gap of 100 bp
* 20355 21083: contig of 729 bp in length
* 21084 21183: gap of 100 bp
* 21184 21910: contig of 727 bp in length
* 21911 22010: gap of 100 bp
* 22011 22738: contig of 728 bp in length
* 22739 22838: gap of 100 bp
* 22839 23553: contig of 715 bp in length
* 23554 23653: gap of 100 bp
* 23654 24374: contig of 721 bp in length
* 24375 24474: gap of 100 bp
* 24475 25193: contig of 719 bp in length
* 25194 25293: gap of 100 bp
* 25294 26037: contig of 744 bp in length
* 26038 26137: gap of 100 bp
* 26138 26860: contig of 723 bp in length
* 26861 26960: gap of 100 bp
* 26961 27665: contig of 705 bp in length
* 27666 27765: gap of 100 bp
* 27766 28471: contig of 706 bp in length
* 28472 28571: gap of 100 bp
* 28572 29282: contig of 711 bp in length
* 29283 29382: gap of 100 bp
* 29383 30106: contig of 724 bp in length
* 30107 30206: gap of 100 bp
* 30207 30896: contig of 690 bp in length
* 30897 30996: gap of 100 bp
* 30997 31719: contig of 723 bp in length
* 31720 31819: gap of 100 bp
* 31820 32532: contig of 713 bp in length
* 32533 32632: gap of 100 bp

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* 32633 33342: contig of 710 bp in length
* 33343 33442: gap of 100 bp
* 33443 34165: contig of 723 bp in length
* 34166 34265: gap of 100 bp
* 34266 34973: contig of 708 bp in length
* 34974 35073: gap of 100 bp
* 35074 35773: contig of 700 bp in length
* 35774 35873: gap of 100 bp
* 35874 36586: contig of 713 bp in length
* 36587 36686: gap of 100 bp
* 36687 37406: contig of 720 bp in length
* 37407 37506: gap of 100 bp
* 37507 38215: contig of 709 bp in length
* 38216 38315: gap of 100 bp
* 38316 39042: contig of 727 bp in length
* 39043 39142: gap of 100 bp
* 39143 39874: contig of 732 bp in length
* 39875 39974: gap of 100 bp
* 39975 40698: contig of 724 bp in length
* 40699 40798: gap of 100 bp
* 40799 41486: contig of 688 bp in length
* 41487 41586: gap of 100 bp
* 41587 42300: contig of 714 bp in length
* 42301 42400: gap of 100 bp
* 42401 43019: contig of 619 bp in length
* 43020 43119: gap of 100 bp
* 43120 43834: contig of 715 bp in length
* 43835 43934: gap of 100 bp
* 43935 44656: contig of 722 bp in length
* 44657 44756: gap of 100 bp
* 44757 45441: contig of 685 bp in length

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Query Match 5.5%: Score 138; DB 2: Length 69215;

Best Local Similarity 100.0%: Pred. No. 5.2e-58; Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 70 CTTGACGTTGCGGCGCCCTCCTACCTGCGCTGTCACAGCCCGGTGCGCCTTGAGCCCTTT 129
DB 49068 CTTGACGTTGCGGCGCCCTCCTACCTGCGCTGTCACAGCCCGGTGCGCCTTGAGCCCTTT 49069
QY 130 TCTGAGAGGAGGAGCGCTGTCTTCCCGTCAGAGAGCTTGAGGAGGACACCTGAC 189
DB 49008 TCTGAGAGGAGGAGCGCTGTCTTCCCGTCAGAGAGCTTGAGGAGGACACCTGAC 48949
QY 190 CTGACGACGCTTGCCCTT 207
DB 48948 CTGACGACGCTTGCCCTT 48931

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Search completed: May 27, 2003, 11:08:57
Job time : 7346 secs

Search completed: May 27, 2003, 09:06:15
Job time : 568 secs

RESULT 2

ABL80248/c
ID ABL80248 standard; cDNA; 302 BP.

XX ABL80248;

DT 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:3226.

KM Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

OS Homo sapiens.

PN W0200192581-A2.

PD 06-DEC-2001.

XX 29-MAY-2001: 2001WO-US17756.

PR 26-MAY-2000: 2000US-207484P.

XX (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI: 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

XX polypeptide -

PS Claim 1; SEQ ID 3226; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour

CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence

CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to

CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell

CC population of (II), or antigen presenting cells that express (II).

CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to

CC (S1) can be used for detecting ovarian cancer in a patient's biological

CC sample preferably serum or ovarian tissue. The method comprises

CC contacting a biological sample from a patient with (IV), detecting the

CC amount of polynucleotide hybridising to (IV) and comparing the amount to

CC a predetermined cutoff value and thereby detecting ovarian cancer in the

CC patient, where the amount of polynucleotide hybridising to (IV) is

CC detected preferably by polymerase chain reaction (PCR). (I) comprising

CC (II) and/or (II) is useful for stimulating and/or expanding T cells

CC with (III) or (II). (III) is useful in design and preparation of

CC ribozyme molecules for inhibiting expression of the tumour polypeptides

CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour cDNA library using well known

XX techniques.

XX Sequence 302 BP; 59 A; 96 C; 108 G; 39 T; 0 other;

SO Query Match 4.0%; Score 101; DB 24; Length 302;

Best Local Similarity 100.0%; Pred. No. 9.9e-36;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2096 AGAATTTGTCGCTTCGCTGACGAGGCGCCGACGTGACGACCCAGGTGGCCAGG 2155

DB 260 AGAATTTGTCGCTTCGCTGACGAGGCGCCGACGTGACGACCCAGGTGGCCAGG 201

OY 2156 CTGCGAAGGCAATCACCCTTCACAGATGCCCTCAACTGTG 2196

DB 200 CTGCGAAGGCAATCACCCTTCACAGATGCCCTCAACTGTG 160

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 08:59:22 ; Search time 95 Seconds
(without alignments)
8151.146 Million cell updates/sec

Title: US-09-993-731-10

Perfect score: 2525
Sequence: 1 ctctgggctgtgcccgtggcc.....cgcattctctctccacacaga 2525

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 100

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

No matches found		

Search completed: May 27, 2003, 11:58:01
Job time : 98 secs


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; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701

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Search completed: May 27, 2003, 13:57:18
Job time : 341 secs

GenCore version 5.1.4-P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 08:51:45 ; Search time 3520 Seconds
(without alignments)
11617.501 Million cell updates/sec

Title: US-09-993-731-10

Perfect score: 2525
Sequence: 1 ctctggcgtgtgcccgtgccc.....cgcatctctctcccaaga 2525

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 100

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	703	27.8	817	14	BQ230076
2	680	26.9	1096	13	BM463971
3	491	19.4	970	14	BM903924
4	486	19.2	1170	13	BM477754
5	449	17.8	929	14	BM960372
6	388	15.4	682	10	BM407508

7	236	9.3	1784	14	B0057501
8	194	7.7	492	13	BM193972
9	180	7.1	421	10	BE383502
10	180	7.1	1101	12	BE314727
11	167	6.6	443	9	AI733922
12	167	6.6	503	9	AI820902
13	167	6.6	543	12	BF111950
14	148	5.9	699	12	BG392570
15	136	5.4	506	9	AI821538
16	136	5.4	506	9	AI821587
17	132	5.2	476	12	BG474073
18	131	5.2	347	14	BQ379444
19	121	4.8	483	12	BF954610
20	117	4.6	477	9	AI570434
21	101	4.0	302	9	AA293771

ALIGNMENTS

RESULT 1
BQ230076
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LRAM13289 row: 1 column: 13
High quality sequence stop: 687.
Location/Qualifiers
1..817
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6045468"
/clone_id="NIH-MGC-92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: PCMV-SPOK6; Site:1; Noti:
Site:2; Salt: Cloned unidirectionally; Oligo off primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."

BASE COUNT 165 a 254 c 287 g 110 t 1 others

Query Match 27.8%, Score 703; DB 14; Length 817;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1519 GCGGACAGCTGCTGGAGAGGCGCAAGACCTGCTGACATTCACATGCCCCGAGAGG 1578
|||||
DB 1 GCGGACAGCTGCTGGAGAGGCGCAAGACCTGCTGACATTCACATGCCCCGAGAGG 60
|||||
QY 1579 CCGGAGATTCAGAGGCTGCTGAGGCGGCTGCTTCAGAAAGCCCTGAGCTGTCTAGC 1638
|||||

[illegible]

FEATURES		High quality sequence stop: 662.	
Source		Location/Qualifiers	
	1..1096		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:533988"		
	/clone_lib="NIH MGC 72"		
	/tissue_type="melanotic melanoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: Skin; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."		
BASE COUNT	217 a 371 c 362 g 146 t		
ORIGIN			
Query Match	26.9%; Score 680; DB 13; Length 1096;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches 730; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
QY	1432 TCCACGTGTCCTCCGCGGACACACACATGAGACATGAAGACACACATGGGCGCGTGGCC	1491	
Db	26 TCCACGTGTCCTCCGCGGACACACATGGGACATGAAGACACACATGGGCGCGTGGCC	85	
QY	1492 ACTATGAGAGAGAACTGAGGCTGCCACAGCGGACACTGTCTGGAGAGAGCCCAAGACCTGGC	1551	
Db	86 ACTATGAGAGAGAACTGAGGCTGCCACAGCGGACACTGTCTGGAGAGAGCCCAAGACCTGGC	145	
QY	1552 TGAACATTGACATGTCCCGCGAGAGAGCGCGCGATGCTTACGACCTCTGTGGCCCGTGGCT	1611	
Db	146 TGAACATTGACATGTCCCGCGAGAGCGCGCGGATGCTTACGACCTCTGTGGCCCGTGGCT	205	
QY	1612 TCCAGAAAGCGCTCAGCTGTGCTCTGACAGAGGCCACAGCGTGCCTCAGAGGACAGTCT	1671	
Db	206 TCCAGAAAGCGCTCAGCTGTGCTCTGACAGAGGCCACAGCGTGCCTCAGAGGACAGTCT	265	
QY	1672 TGCAGCATCTCCATACCGTGTGACGCTGTGACGCTGTGACGCCCCAGAGGCCCCCTGAGACCGAAA	1731	
Db	266 TGCAGCATCTCCATACCGTGTGACGCTGTGACGCTGTGACGCCCCAGAGGCCCCCTGAGACCGAAA	325	
QY	1732 CCAAGACTGCGGGAGCTCAGCTGTAGCTGAAAGATGAAGATGAAGAGAGACAGAGCGGAGAGG	1791	
Db	326 CCAAGACTGCGGGAGCTCAGCTGTAGCTGAAAGATGAAGATGAAGAGAGAGAGCGGAGAGG	385	
QY	1792 CGGACGACCAAGCGGAGAGCGAAGCCCTGAGAGGCCGCGGAGGTGAGCTCTCAGAGAGCG	1851	
Db	386 CGGACGACCAAGCGGAGAGCGAAGCCCTGAGAGGCCGCGGAGGTGAGCTCTCAGAGAGCG	445	
QY	1852 AGGAGCAACACCATGGCCCTGACCCCGGACGCTGTGAGAGAGAGAGAGACTTCAAGGCGCACCC	1911	
Db	446 AGGAGCAACACCATGGCCCTGACCCCGGACGCTGTGAGAGAGAGAGAGACTTCAAGGCGCACCC	505	
QY	1912 TGGGCGCGGAGGAGGAGCAAGTGTGAACCGCGCAAAACGACATGGGGGAGACCCCTCTCG	1971	
Db	506 TGGGCGCGGAGGAGGAGCAAGTGTGAACCGCGCAAAACGACATGGGGGAGACCCCTCTCG	565	
QY	1972 ACCGAGCCTTCGATCGAGGGCCACGCTGCGCGCGGTCCAGAGACCTTGTGAGGACAGGCGCACCC	2031	
Db	566 ACCGAGCCTTCGATCGAGGGCCACGCTGCGCGCGGTCCAGAGACCTTGTGAGGACAGGCGCACCC	625	
QY	2032 CCCTTAACCTCGGGGACTACGTGTGGCTGTGAACCTGTGCACAGAGGCGCTGCACATACGGGC	2091	
Db	626 CCCTTAACCTCGGGGACTACGTGTGGCTGTGAACCTGTGCACAGAGGCGCTGCACATACGGGC	685	
QY	2092 ATCTAGAAATGTCTCGCTTCCGTGCTGAGACACAGGGGCGCAGTGGAGACCCAGGTGGCC	2151	
Db	686 ATCTAGAAATGTCTCGCTTCCGTGCTGAGACACAGGGGCGCAGTGGAGACCCAGGTGGCC	745	
QY	2152 AGGCGTCGGCAA 2162		
Db	746 AGGCGTCGGCAA 756		

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RESULT 3
BM903924      970 bp  mRNA  linear  EST 12-MAR-2002
LOCUS         AGENCOURT_6695791 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5492426
DEFINITION    5', mRNA sequence.
ACCESSION     BM903924
VERSION       BM903924.1 GI:19353843
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1 (bases 1 to 970)
AUTHORS       NIH-MGC http://mgi.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapds-remail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.lnl.gov
              Plate: LLM12114 row: 1 column: 03
              High quality sequence stop: 668.
              Location/Qualifiers
                1. 970
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_1ib="IMAGE:5492426"
                /clone_1ib="NIH_MGC_67"
                /tissue_type="retinoblastoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: eye; Vector: PCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.75 kb. Library constructed by Life
                Technologies."
                Technology="Life"

BASE COUNT    203 a 335 c 312 g 119 t 1 others
ORIGIN
Query Match    19.4%; Score 491; DB 14; Length 970;
Best Local Similarity 99.8%; Pred. No. 3.2e-227;
Matches 541; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1844 AGAGAGCGAGAGACACCGATGAGCCCGCAGCTGAGAGAGAGAGAGAGCTTCA 1903
    |||
    1 AGAGAGCGAGAGACACCGATGAGCCCGCAGCTGAGAGAGAGAGAGAGCTTCA 60
QY 1904 GGGGACCTGGGCGGGGGAAGGAGCAAGTGAACCGGCGAAGACATGGGGGAGAC 1963
    |||
    61 GGGGACCTGGGCGGGGGAAGGAGCAAGTGAACCGGCGAAGACATGGGGGAGAC 120
QY 1964 CCTGCTGACACCGATGAGCGAGGCGACGCTGCCCGCGCTCCAGAGACTTGTGAGCA 2023
    |||
    121 CCTGCTGACACCGATGAGCGAGGCGACGCTGCCCGCGCTCCAGAGACTTGTGAGCA 180
QY 2024 GGGGACCGCCCTTAACCTGGGAGCTACTGTGGCTGAGACACCTGACAGAGCCTGCAA 2083
    |||
    181 GGGGACCGCCCTTAACCTGGGAGCTACTGTGGCTGAGACACCTGACAGAGCCTGCAA 240
QY 2084 CTACGGGATCTAGAAATTTGCTGCTGCTGCTGAGACACAGGGGCGCGAGTGGACACCC 2143
    |||
    241 CTACGGGATCTAGAAATTTGCTGCTGCTGCTGAGACACAGGGGCGCGAGTGGACACCC 300
QY 2144 AGGTGGCCAGGCGTCCGAAGCATCACCCCTCCACAGATGCCCTCAATGTGGCCACTT 2203
    |||
    301 AGGTGGCCAGGCGTCCGAAGCATCACCCCTCCACAGATGCCCTCAATGTGGCCACTT 360
QY 2204 CGAGTGGCTGAGCTGCTGTTGAACGGGGGCGTCCGTGACCTCCGACTCGCAAGAGG 2263
    |||
    361 CGAGTGGCTGAGCTGCTGTTGAACGGGGGCGTCCGTGACCTCCGACTCGCAAGAGG 420

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QY 2264 CCTGAGCCCGCTGAGAGACGCTGAGCAGTGGTGAACCTGTAACGACAGAGACCTGAGACT 2323
    |||
    421 CCTGAGCCCGCTGAGAGACGCTGAGCAGTGGTGAACCTGTAACGACAGAGACCTGAGACT 480
QY 2324 GAGACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2383
    |||
    481 GAGACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 2384 AG 2385
    ||
    Db 541 AG 542

RESULT 4
BM477754      1170 bp  mRNA  linear  EST 05-FEB-2002
LOCUS         AGENCOURT_6485291 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555018
DEFINITION    5', mRNA sequence.
ACCESSION     BM477754
VERSION       BM477754.1 GI:18526796
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1 (bases 1 to 1170)
AUTHORS       NIH-MGC http://mgi.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapds-remail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.lnl.gov
              Plate: LLM12274 row: 1 column: 03
              High quality sequence stop: 548.
              Location/Qualifiers
                1. 1170
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_1ib="IMAGE:5555018"
                /clone_1ib="NIH_MGC_71"
                /tissue_type="leiomyosarcoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 2.1 kb."
                Technology="Life"

BASE COUNT    240 a 420 c 332 g 177 t 1 others
ORIGIN
Query Match    19.2%; Score 486; DB 13; Length 1170;
Best Local Similarity 99.8%; Pred. No. 9e-225;
Matches 536; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1849 GCGAGAGACACCGATGAGCGCTGACCCCGAGCTGAGAGAGAGAGAGAGCTTCAAGGCC 1908
    |||
    46 GCGAGAGACACCGATGAGCGCTGACCCCGAGCTGAGAGAGAGAGAGAGCTTCAAGGCC 105
QY 1909 ACCTGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1968
    |||
    106 ACCTGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 165
QY 1969 TGCACGAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2028
    |||
    166 TGCACGAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 225
QY 2029 ACCCCCTTAACCTCGGAGACTGCTGCTGAGACACCTTGCAGAGAGAGCTTGCAATTCG 2088
    |||

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Db 226 ACCCCCTTAACCTCTGGGAGCTACTGTGGCTGAGACACTCTGACGAGAGCCTGCAACTAG 285
 QY 2089 GGCATCTAGAAATTTGTCCTCTCTGCTGAGACAGAGGGGCGGACAGTACAGACCCAGGTG 2148
 Db 286 GGCATCTAGAAATTTGTCCTCTCTGCTGAGACAGAGGGGCGGACAGTACAGACCCAGGTG 345
 QY 2149 GCGAGGGCTGGCAAGGACATCACCCCTCCACAGATGCTCCCTCACTGAGCCACTTGCAGG 2208
 Db 346 GCGAGGGCTGGCAAGGACATCACCCCTCCACAGATGCTCCCTCACTGAGCCACTTGCAGG 405
 QY 2209 TGGCTAGCTGCTGCTTGAACGGGGGGCGTCCCTGACCCCTCCGACACTGAAAGGCGCTCA 2268
 Db 406 TGGCTAGCTGCTGCTTGAACGGGGGGCGTCCCTGACCCCTCCGACACTGAAAGGCGCTCA 465
 QY 2269 GCGCGCTGGAGAGCGCTGCGAGCAGTGGTGAAGCTGTACCGAGAGGACCTGAGACTGAGAG 2228
 Db 466 GCGCGCTGGAGAGCGCTGCGAGCAGTGGTGAAGCTGTACCGAGAGGACCTGAGACTGAGAG 525
 QY 2329 CCGGCGAGAGGCGCAGGCGCATGAGATGCTGCTCCAGGCGGCTGCTCGGCGCAAG 2385
 Db 526 CCGGCGAGAGGCGCAGGCGCATGAGATGCTGCTCCAGGCGGCTGCTCGGCGCAAG 582
 RESULT 5
 B0960372 929 bp mRNA linear EST 21-ANG-2002
 LOCUS AGEMCOURT_8923052 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6472657
 DEFINITION 5', mRNA sequence.
 ACCESSION B0960372
 VERSION B0960372.1 GI:22375850
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 929)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Consortium
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM14006 row: p column: 02
 High quality sequence stop: 662.
 Location/Qualifiers
 1..929
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6472657"
 /clone_lib="NIH_MGC_71"
 /tissue_type="telomysarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb.
 BASE COUNT 191 a 281 c 306 g 149 t 2 others
 ORIGIN
 Query Match 17.8% Score 449: DB 14: Length 929:
 Best Local Similarity 99.8% Pred. No. 8.4e-207;
 Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
 QY 633 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 692
 Db 243 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 302
 QY 693 AGGGCTGGGCGACATCTGCGCGCACCCACCTGAGACATCTATGACCACTGCGAGTCCAGG 752

Db 303 AGGGCTGGGCGACATCTGCGCGCACCCACCTGAGCATCTATGACCACTGCGAGTCCAGG 362
 QY 753 GATGCTTGTGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 812
 Db 363 GATGCTTGTGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 422
 QY 813 TTGGAGGGAGACACTGCGCGCAGGAGAGCTGATGATGAGACCCGCTCATCTCAAC 872
 Db 423 CTGAGAGGGAGACACTGCGCGCAGGAGAGCTGATGATGAGACCCGCTCATCTCAAC 482
 QY 873 CTGGGCTCATCTTGGAGAGCTGCGAGCAGACAGCCCTGTCAGAGATTACTTCAAGAG 932
 Db 483 CTGGGCTCATCTTGGAGAGCTGCGAGCAGACAGCCCTGTCAGAGATTACTTCAAGAG 542
 QY 933 AGCATCTTCTTGGGAGCAGACAGACACCTTATGAGAGACCTTATCGCGCGCTACAG 992
 Db 543 AGCATCTTCTTGGGAGCAGACACCTTATGAGAGACCTTATCGCGCGCTACAG 602
 QY 993 CTGGGACCATCTCAGTGGCGCGCGCGCGCAGCACTCCAGGCTATGCGCTTGGAGGTT 1052
 Db 603 CTGGGACCATCTCAGTGGCGCGCGCGCGCAGCACTCCAGGCTATGCGCTTGGAGGTT 662
 QY 1053 GCGCGGAGTGTGGGAGCAGACCATGAGGAGCGGTTGATGAGAGAGAGTGGTGGTT 1112
 Db 663 GCGCGGAGTGTGGGAGCAGACCATGAGGAGCGGTTGATGAGAGAGAGTGGTGGTT 722
 QY 1113 ATTGCACAGTCTCTCCAGA 1132
 Db 723 ATTGCACAGTCTCTCCAGA 742
 RESULT 6
 BE407508 682 bp mRNA linear EST 21-JUL-2000
 LOCUS 601300344F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3630371 5',
 DEFINITION mRNA sequence.
 ACCESSION BE407508
 VERSION BE407508.1 GI:9343958
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 682)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
 Plate: LLM018 row: g column: 12
 High quality sequence stop: 661.
 Location/Qualifiers
 1..682
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3630371"
 /clone_lib="NIH_MGC_21"
 /tissue_type="choriocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: placenta; Vector: pORF7; Site: 1: XhoI;
 Site: 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACAGG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit

BASE COUNT 150 a 200 c 246 g 86 t
 ORIGIN (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 15.4% Score 388; DB 10; Length 682;
 Best Local Similarity 99.8%; Pred. No. 3.6e-177;
 Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1468 AGGACACCATGGGCGCGCTGCTGCTATGAGAGAGAACTGAGGCTGGCGAGCGCAACG 1527
 DB 1 AGGACACCATGGGCGCGCTGCTGCTATGAGAGAGAACTGAGGCTGGCGAGCGCAACG 60
 QY 1528 TGTGAG 1587
 DB 61 TGTGAG 120
 QY 1588 CCTAG 1647
 DB 121 CCTAG 180
 QY 1648 GTGCCAGCTGACAG 1707
 DB 181 GTGCCAGCTGACAG 240
 QY 1708 CCCAG 1767
 DB 241 CCCAG 300
 QY 1768 ATGAG 1827
 DB 301 ATGAG 360
 QY 1828 GGGAG 1887
 DB 361 GGGAG 420
 QY 1888 AGGACAG 1906
 DB 421 AGGACAG 439

RESULT 7 1784 bp mRNA linear EST 29-MAR-2002
 LOCUS B0057501
 DEFINITION AGENCOURT_6739552 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813130
 ACCESSION B0057501
 VERSION B0057501.1 GI:19816841
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1784)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@ncl.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM2064 row: k column: 19
 High quality sequence stop: 330.
 Location/Qualifiers
 1..1784
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5813130"

FEATURES

Source
 1..1784
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5813130"

/clone.lib="NIH_MGC_99"
 /issue_type="Lymphoma, cell line"
 /lab_host="PH10B (phage-resistant)"
 /note="Organ: Lymph; Vector: pORF1; Site: 1; XhoI; Site: 2;
 ECORI; cDNA made by oligo-dT priming. Directionally cloned
 into ECORI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Size: selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 415 a 603 c 458 g 282 t 26 others
 ORIGIN

Query Match 9.3% Score 236; DB 14; Length 1784;
 Best Local Similarity 99.2%; Pred. No. 3e-103;
 Matches 386; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1849 GCGAG 1908
 DB 30 GCGAG 89
 QY 1909 ACTGGGCGCGGAG 1968
 DB 90 ACTGGGCGCGGAG 149
 QY 1969 TGACACGAG 2028
 DB 150 TGACACGAG 209
 QY 2029 ACCCGCTTAACCGTGGAG 2088
 DB 210 ACCCGCTTAACCGTGGAG 269
 QY 2089 GGCATCTAGAAATTTGCGCTTCTGCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 2148
 DB 270 GGCATCTAGAAATTTGCGCTTCTGCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 329
 QY 2149 GGCAG 2208
 DB 330 GGCAG 389
 QY 2209 TGGCTGAGCTGCTGCTTGAACGGGGGCG 2237
 DB 390 TGGCTGAGCTGCTGCTTGAACGGGGGCG 418

RESULT 8 492 bp mRNA linear EST 13-DEC-2001
 LOCUS BM193972
 DEFINITION TCAP1E5856 Pediatric pre-B cell acute lymphoblastic leukemia
 BAYLOR-HESC project-TCBA Homo sapiens cDNA clone TCAP1E5856, mRNA
 sequence.
 ACCESSION BM193972
 VERSION BM193972.1 GI:17652620
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 492)
 AUTHORS Wei, Y., Tsang, T.T.M., Mel, G., Ku, J.M., Ali-Osman, F.R., Jr.,
 Guareatane, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
 TITLE Pediatric leukemia cDNA sequencing project (2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Dr. Judith F. Margolin
 Texas Children's Cancer Center and Human Genome Sequencing Center
 at Baylor College of Medicine
 1102 Bates MC3-3320 Houston, TX 77030, USA
 Tel: 832-824-4536
 Fax: 832-825-4038
 Email: clones@txccc.org


```

source
1. .j101
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone-"IMAGE:4130611"
/clone_1lb="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="PH10B (phage-resistant)"
/ecori_cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald W. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT      318 a      340 g      132 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 4.7e-76;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 633 CAGACCAGCAGCCAGTCAGCTGGACTGGACATTCCTCGGCCAGCACACAGCAGCTGCAG 692
|||||
Db 252 CAGACAGCAGCAGCAGTACCTGGAGCTGGACATTCCTCGGCCAGCACACAGCAGCTGCAG 311
|||||

OY 693 AGGCGCTGGGGCCACCATCGGCGCCGACCCACCTGTGACATCTATGACACTGGCAGTCGAG 752
|||||
Db 312 AGGGCGCTGGGGCCACCATCGGCGCCGACCCACCTGTGACATCTATGACACTGGCAGTCGAG 371
|||||

OY 753 GATGCTTTTGCTGTCAGGACGACAGCGTGCCTTTGAGAAGAGCTGGCTATTGTGATGAGAG 812
|||||
Db 372 GATGCTTTTGCTGTCAGGACGACAGCGTGCCTTTGAGAAGAGCTGGCTATTGTGATGAGAG 431
|||||

RESULT 11
LOCUS AT1733922/c
DEFINITION IMAGE:726311 5' similar to YR.Q13006 Q13006 I KAPPA BR.; mRNA
sequence.
ACCESSION AT1733922
VERSION AT1733922.1 GI:5055035
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other_ESTs: zt55hl2.s1
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: Washn-NCI human EST Project
This read has been verified (found to hit its original self in the
correct orientation)
Possible reversed clone: similarity on wrong strand
Insert length: 633 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 442.
Location/Qualifiers
1. .443
/organism="Homo sapiens"
/db_xref="GDB:5938403"
/db_xref="taxon:9606"
/clone-"IMAGE:726311"
/clone_1lb="Soares ovary tumor NbHOT"
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	/sex="Female"	/tissue.type="ovarian tumor"
	/lab_host="TDH10B (ampicillin resistant)"	/note="Organ: ovary; Vector: p7T73D (Pharmacia) with a modified polylinker; Site_1: Not I - o19o(dt) primer [5' GTTACCAATCTGAAGTCGACGGCGCGGTGTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. ID."
BASE COUNT	98 a 141 c 141 g 62 t 1 others	
ORIGIN		
Query Match	6.6%; Score 167; DB 9; Length 443;	
Best Local Similarity	100.0%; Pred. No. 8.7e-70;	
Matches 167; Conservative	0; Mismatches 0; Indels 0; Gaps 0.	
OY	2096 AGAATTGCCGCTTGCTCCTGTGCAGCACCGGGGCGCCAGTGTGACGACCAGGTGGCCAGG 2155	
Db	262 AGAAATGTCCGCTCTGTGCACCGGGGCGCCAGTGTGACCAACCCAGTGGCCAGG 203	
OY	2156 CTCGGAAGCATACCCCCCTCCAGATGCCCTCAACTGTGGCCACTTCGAGGTGGCTGA 2215	
Db	202 CTGGGAAGCATACCCCCCTCCAGATGCCCTCAACTGTGGCCACTTCGAGGTGGCTGA 143	
OY	2216 GCTGCTCTTTGAACGGGGGCGCTCGTACCCCTCCGCACTGGAAAG 2262	
Db	142 GCTGCTCTTTGAACGGGGGCGCTCGTACCCCTCCGCACTGGAAAG 96	
RESULT 12		
A1820902/c	503 bp mRNA linear; EST 24-OCT-2000	
LOCUS	ZL39d01.y5 Soares ovary tumor NBHOT Homo sapiens cDNA clone	
DEFINITION	IMAGE:724705 5' similar to TR:Q13006 Q13006 I KAPA BR.; mRNA sequence.	
ACCESSION	A1820902 GI:5439981	
VERSION	A1820902.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 503)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Other-ESTS: ZL39d01.x5 Contact: Robert Strausberg, Ph.D. Email: cgaps@email.nih.gov This clone is available royally-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESSEQUENCE of a previously sequenced human clone Original clone citation: Mashu-NCI human EST Project This read has been verified (found to hit its original self in the correct orientation) Putative full length read The vector to vector length is 581 Possible reversed clone: similarity on wrong strand Insert Length: 639 Std Error: 0.00 Seq primer: -40RP from Gibco High quality sequence stop: 465. Location/Qualifiers 1..503 /organism="Homo sapiens" /db_xref="GDB:5936350" /db_xref="taxon:9606" /clone="IMAGE:724705" /clone_1lb="Soares ovary tumor NBHOT" /sex="female"	
FEATURES		
Source		


```

/tissue-type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCTTACCATCTGACGAGGAGGCGCGGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73D vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
BASE COUNT      107 a      168 c      152 g      76 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 8.8e-70; Length 503;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2096 AGAATTGTCGCTCTCTGTCGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 2155
262 AGAATTGTCGCTCTCTGTCGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 203
QY 2156 CTGGCAAGCATCACCCCTCCAGATGCCCTCACTGTGGCCACTTGCAGTGGCTGA 2215
Db 202 CTGGCAAGCATCACCCCTCCAGATGCCCTCACTGTGGCCACTTGCAGTGGCTGA 143
QY 2216 GCTGCTGTTGACGAGGGGGGCGTCCTCACCCCTCCAGTGGCAAGG 2262
Db 142 GCTGCTGTTGACGAGGGGGGCGTCCTCACCCCTCCAGTGGCAAGG 96

RESULT 13
LOCUS      Bf111950      543 bp      mRNA      linear      EST 20-OCT-2000
DEFINITION 7139c01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3523585 3' similar to TR:09UGJ2 09UGJ2 IKAPPAHR.;, mRNA
sequence.
Bf111950
EST.
Bf111950.1 GI:10941729
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 543)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-rt@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 543
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3523585"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pec (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneids: Soares NBHP pool 1:
309384-310919, 323208-325895 Soares NBHP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -

/tissue-type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCTTACCATCTGACGAGGAGGCGCGGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73D vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
BASE COUNT      91 a      161 c      172 g      119 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 8.9e-70; Length 543;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2096 AGAATTGTCGCTCTCTGTCGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 2155
Db 320 AGAATTGTCGCTCTCTGTCGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 379
QY 2156 CTGGCAAGCATCACCCCTCCAGATGCCCTCACTGTGGCCACTTGCAGTGGCTGA 2215
Db 380 CTGGCAAGCATCACCCCTCCAGATGCCCTCACTGTGGCCACTTGCAGTGGCTGA 439
QY 2216 GCTGCTGTTGACGAGGGGGGCGTCCTCACCCCTCCAGTGGCAAGG 2262
Db 440 GCTGCTGTTGACGAGGGGGGCGTCCTCACCCCTCCAGTGGCAAGG 486

RESULT 14
LOCUS      BG392570      699 bp      mRNA      linear      EST 12-MAR-2001
DEFINITION 602410786F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4539789 5',
mRNA sequence.
BG392570
EST.
BG392570.1 GI:13286018
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 699)
AUTHORS    NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-rt@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LHAM10468 row: K column: 22
High quality sequence stop: 578.
Location/Qualifiers
1. 699
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4539789"
/clone_lib="NIH_MGC_92"
/tissue-type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally, oligo-dT primed.
Average insert size 2.5 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: This is a NIH_MGC Library."
BASE COUNT      149 a      221 c      222 g      107 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-60; Length 699;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2007 CAGACCTTGAGAGCGAGGCGCACCCCTTAACCTTCGAGACTACTGTGCGACACCT 2066

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Accession	Sequence	Position
Db		
172	CAGACCTTGTGAGGAGGAGGGCCACCCCTTAACCCCTGGGAACTACTGTGGCTGGACACCT	231
OY	CTGCAGCAGGCGCTTGCAACTACGCGGCATCTAGAAATTGTCGCTTCTGCTGGACACCGG	2126
Db		
232	CTGCACACGAGCGCTGCAACTACGCGGCATCTAGAAATTGTCGCTTCTGCTGGACACCGG	291
OY		
2127	GCGCAGTGGAGCAGCCAGGTGGCCACG	2154
Db		
292	GCGCAGTGGAGCAGCCAGGTGGCCACG	319

RESULT 15
AI821538

LOCUS	AI821538	506 bp	mRNA	linear	EST 24-OCT-2000
DEFINITION	zt39601.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone				

IMAGE:724705 3' similar to TR:Q13006 Q13006 I KAPPA BR. ;, mRNA sequence.
ATG21520

ACCESSION	AI821538
VERSION	AI821538.1
KEYWORDS	GI:5440617 EST.

ORGANISM

REFERENCE
1 (bases 1 to 506)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

This 3' clone is available royalty-free through INM; contact the IMAG Consortium (info@imag.inl.gov) for further information. This read is a RESEQUENCE of a previously sequenced human clone. Original clone citation: see original entry for original citation information

This 3' resequenced clone has no previous 3' data to verify this new read against

Possible reversed clone: similarity on wrong strand

Insert Length: 639 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 463.

FEATURES
source

Location/Qualifiers
1. .506

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/organism="Homo sapiens"
ddb_xref="CDB:5036350"
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/u01/are1- gdb: 00000000
/db_xref="taxon:9606"
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/clone="IMAGE:724705"
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/clone_lib="Soares ovary tumor NbHOT"
/seq="NbHOT"
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sex = female
tissue type =
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/lab_host="DH10B (ampicillin
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/note="Organ: ovary; Vector: PT7T3D (Pha

moalried polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5

TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTT 3'),

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library constructed by Bento Soares and

M. Fatima Bonaldo, "

BASE COUNT	M. Falcina Bonafido.		
ORIGIN			
89 a	143 c	161 g	111 t
			2 others

Query Match 5.4%; Score 136; DB 9; Length 506;

Best Local Similarity 100.0%; Pred. No. 1e-54;

Matches	136;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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QY 2096 AGAATTTGTCGGCTTCCTGCTGACACACGGGGCCGCAGTGGACGACCCAGGTGGCCAGGG 2155

Db 320 AGAAATTCCTCCTGACGACGCGCGCAGTGGACGACCAAGTGGCCAGG 379

Oy	2156	CTGAGAGCATACCCCCCTCCAGCATGCCCGCAACTGGCACAATTCGACGTGGCGA	2215
Db	380	CTGCGAAGGCATCACCCCCCTCCAGCATGCCCGCTCAACTGGCACCTTGAGAGTGGCTGA	439
Oy	2216	GCTCGCTGCTTGAAACGG	2231
Db	440	GCTCGCTGCTTGAAACGG	455

Qy 2156 CTGGGAAGGCATCACCCCTCCACAGATGCCCTCAACTGTGGCCACTTCGAGGTGGCTGA 2215
|||||
Db 380 CTGGGAAGGCATCACCCCTCCACAGATGCCCTCAACTGTGGCCACTTCGAGGTGGCTGA 439

OY	2216	GCTGCTGCTTGAACGG	2231
Db	440	GCTGCTGCTTGAACGG	455

Search completed: May 27, 2003, 11:56:50
Job time : 3565 secs

